# STIC Biotechnology Systems Branch

# RAW SEQUENCE LISTING
## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/550,498A*
Source: *IFWO*
Date Processed by STIC: *3/24/06*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> **http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

# Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _10/550,498A_ |
|---|---|---|

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

**1____Wrapped Nucleics Wrapped Aminos**  The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

**2____Invalid Line Length**  The rules require that a line **not exceed 72** characters in length. This includes white spaces.

**3____Misaligned Amino Numbering**  The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters,** instead.

**4____Non-ASCII**  The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

**5____Variable Length**  Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

**6____PatentIn 2.0 "bug"**  A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

**7____Skipped Sequences (OLD RULES)**  Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

**8____Skipped Sequences (NEW RULES)**  Sequence(s) _____ missing. If **intentional,** please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

**9____Use of n's or Xaa's (NEW RULES)**  Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa,** and which residue **n** or **Xaa** represents.

**10____Invalid <213> Response**  Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

**11____Use of <220>**  Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

**12____PatentIn 2.0 "bug"**  Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

**13____Misuse of n/Xaa**  "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWO

```
 3 <110> APPLICANT: Minchiotti, Gabriella
 4        Persico, Maria
 5        Parisi, Silvia
 7 <120> TITLE OF INVENTION: METHOD FOR PROMOTING DIFFERENTIATION OF STAMINAL CELL
 9 <130> FILE REFERENCE: AE 89363
11 <140> CURRENT APPLICATION NUMBER: US 10/550,498A
12 <141> CURRENT FILING DATE: 2005-09-20
14 <160> NUMBER OF SEQ ID NOS: 42
16 <170> SOFTWARE: PatentIn version 3.3
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 22
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial
23 <220> FEATURE:
24 <223> OTHER INFORMATION: primer nodal F
27 <220> FEATURE:
28 <221> NAME/KEY: primer_bind
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31 <400> SEQUENCE: 1
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37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial
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41 <223> OTHER INFORMATION: Primer nodal R
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45 <221> NAME/KEY: primer_bind
46 <222> LOCATION: (1)..(21)
48 <400> SEQUENCE: 2
49 ggtggggttg gtatcgtttc a                                         21
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 25
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial
57 <220> FEATURE:
58 <223> OTHER INFORMATION: primer alk-4 F
61 <220> FEATURE:
62 <221> NAME/KEY: primer_bind
63 <222> LOCATION: (1)..(25)
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66 aaggatccag gctctgctgt gtgcc                                     25
69 <210> SEQ ID NO: 4
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86 <210> SEQ ID NO: 5
87 <211> LENGTH: 20
88 <212> TYPE: DNA
89 <213> ORGANISM: Artificial
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92 <223> OTHER INFORMATION: primer ActRIIB F
95 <220> FEATURE:
96 <221> NAME/KEY: primer_bind
97 <222> LOCATION: (1)..(20)
99 <400> SEQUENCE: 5
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103 <210> SEQ ID NO: 6
104 <211> LENGTH: 20
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial
108 <220> FEATURE:
109 <223> OTHER INFORMATION: primer ActRIIB R
112 <220> FEATURE:
113 <221> NAME/KEY: primer_bind
114 <222> LOCATION: (1)..(20)
116 <400> SEQUENCE: 6
117 gacctcctga tcagggatac                                20
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121 <211> LENGTH: 24
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial
125 <220> FEATURE:
126 <223> OTHER INFORMATION: primer MLC2v F
129 <220> FEATURE:
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131 <222> LOCATION: (1)..(24)
133 <400> SEQUENCE: 7
134 gccaagaagc ggatagaagg cggg                           24
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139 <212> TYPE: DNA
140 <213> ORGANISM: Artificial
142 <220> FEATURE:
143 <223> OTHER INFORMATION: primer MLC2v R
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RAW SEQUENCE LISTING                    DATE: 03/24/2006
PATENT APPLICATION:   US/10/550,498A        TIME: 17:41:40

Input Set : **A:\persico corrected feb06.ST25.txt**
Output Set: **N:\CRF4\03242006\J550498A.raw**

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146 <220> FEATURE:
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155 <211> LENGTH: 24
156 <212> TYPE: DNA
157 <213> ORGANISM: Artificial
159 <220> FEATURE:
160 <223> OTHER INFORMATION: primer cardiac alphaMHC F
163 <220> FEATURE:
164 <221> NAME/KEY: primer_bind
165 <222> LOCATION: (1)..(24)
167 <400> SEQUENCE: 9
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171 <210> SEQ ID NO: 10
172 <211> LENGTH: 22
173 <212> TYPE: DNA
174 <213> ORGANISM: Artificial
176 <220> FEATURE:
177 <223> OTHER INFORMATION: primer cardiac alphaMHC R
180 <220> FEATURE:
181 <221> NAME/KEY: primer_bind
182 <222> LOCATION: (1)..(22)
184 <400> SEQUENCE: 10
185 ctgctggaga ggttattcct cg                                      22
188 <210> SEQ ID NO: 11
189 <211> LENGTH: 25
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial
193 <220> FEATURE:
194 <223> OTHER INFORMATION: primer HPRT F
197 <220> FEATURE:
198 <221> NAME/KEY: primer_bind
199 <222> LOCATION: (1)..(25)
201 <400> SEQUENCE: 11
202 cctgctggat tacattaaag cactg                                   25
205 <210> SEQ ID NO: 12
206 <211> LENGTH: 25
207 <212> TYPE: DNA
208 <213> ORGANISM: Artificial
210 <220> FEATURE:
211 <223> OTHER INFORMATION: primer HPRT R
214 <220> FEATURE:
215 <221> NAME/KEY: primer_bind
216 <222> LOCATION: (1)..(25)
218 <400> SEQUENCE: 12
219 cctgaagtac tcattatagt caagg                                   25
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RAW SEQUENCE LISTING                    DATE: 03/24/2006
PATENT APPLICATION:  US/10/550,498A     TIME: 17:41:40

Input Set : A:\persico corrected feb06.ST25.txt
Output Set: N:\CRF4\03242006\J550498A.raw

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231 <220> FEATURE:
232 <221> NAME/KEY: primer_bind
233 <222> LOCATION: (1)..(27)
235 <400> SEQUENCE: 13
236 gtaagtcgct tattaaaact tgctgtc                              27
239 <210> SEQ ID NO: 14
240 <211> LENGTH: 27
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial
244 <220> FEATURE:
245 <223> OTHER INFORMATION: mut Asn63-Ile
248 <220> FEATURE:
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250 <222> LOCATION: (1)..(27)
252 <400> SEQUENCE: 14
253 gacagcaagt tttaataagc gacttac                              27
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257 <211> LENGTH: 38
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial
261 <220> FEATURE:
262 <223> OTHER INFORMATION: mut Gly71-Asn
265 <220> FEATURE:
266 <221> NAME/KEY: primer_bind
267 <222> LOCATION: (1)..(38)
269 <400> SEQUENCE: 15
270 cttgctgtct gaatggaaac acttgcatcc tggggtcc                  38
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274 <211> LENGTH: 38
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial
278 <220> FEATURE:
279 <223> OTHER INFORMATION: mut Gly71-Asn
282 <220> FEATURE:
283 <221> NAME/KEY: primer_bind
284 <222> LOCATION: (1)..(38)
286 <400> SEQUENCE: 16
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290 <210> SEQ ID NO: 17
291 <211> LENGTH: 23
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial
295 <220> FEATURE:
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*[handwritten annotation:] This does not explain the source of genetic material in the sequence. See item 11 on Even Summary Sheet.*

*[handwritten annotation:] same error*

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296 <223> OTHER INFORMATION: mut Thr72-Ala
299 <220> FEATURE:
300 <221> NAME/KEY: primer_bind
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309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial
312 <220> FEATURE:
313 <223> OTHER INFORMATION: mut Thr72-Ala
316 <220> FEATURE:
317 <221> NAME/KEY: primer_bind
318 <222> LOCATION: (1)..(23)
320 <400> SEQUENCE: 18
321 ccaggatgca agcccctcca ttc                                    23
324 <210> SEQ ID NO: 19
325 <211> LENGTH: 29
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327 <213> ORGANISM: Artificial
329 <220> FEATURE:
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333 <220> FEATURE:
334 <221> NAME/KEY: primer_bind
335 <222> LOCATION: (1)..(29)
337 <400> SEQUENCE: 19
338 cttgcatcct gggggccttc tgtgcctgc                              29
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344 <213> ORGANISM: Artificial
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347 <223> OTHER INFORMATION: mut Ser77-Ala
350 <220> FEATURE:
351 <221> NAME/KEY: primer_bind
352 <222> LOCATION: (1)..(29)
354 <400> SEQUENCE: 20
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360 <212> TYPE: DNA
361 <213> ORGANISM: Artificial
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364 <223> OTHER INFORMATION: mut Phe78-Ala
367 <220> FEATURE:
368 <221> NAME/KEY: primer_bind
369 <222> LOCATION: (1)..(31)
371 <400> SEQUENCE: 21
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*Please correct these types of
errors in subsequent sequences*

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